IN THE ABSTRACT:

Please renumber the Abstract page from page "85" to --113--.

REMARKS

The specification has been amended to provide sequence identifiers. Applicants' amendments do not introduce new matter.

The Examiner has requested that a Sequence Listing be provided. Applicants submit this Preliminary Amendment and Response to provide as a separate part of the disclosure, a "Sequence Listing" pursuant to 37 C.F.R. §§ 1.821-1.825. Applicants submit herewith in paper copy and on floppy disk the Sequence Listing in computer readable form. The contents of the paper and computer readable copies are the same and include no new matter.

Dated: July 12, 2002

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APPENDIX I

MARKED-UP VERSION OF SPECIFICATION'S REPLACEMENT PARAGRAPHS

The following is a marked-up version of the specification's replacement paragraphs pursuant to 37 C.F.R. §1.121(b) with markings showing changes made herein to the previous version of record of the specification.

IN THE SPECIFICATION

On page 8, please delete the paragraphs beginning on line 23 and ending on line 31, and replace with the following paragraphs:

Figure 15 shows the nucleic acid sequence of the promoter region P6 of gene 6 (SEQ ID NO: 25), with an inverted repeat indicated by highlight (SEQ ID NO: 26). The BLAST result of the sequence blasted against its reverse complementary sequence is also shown.

Figure 16 shows the nucleic acid sequence of the promoter region P14 of gene 14 (SEQ ID NO: 27), with an inverted repeat indicated by highlight (SEQ ID NO: 28). The BLAST result of the sequence blasted against its reverse complementary sequence is also shown.

Figure 17 shows the nucleic acid sequence of the promoter region P16 of gene 16 (SEQ ID NO: 29), with an inverted repeat indicated by highlight (SEQ ID NO: 30). The BLAST result of the sequence blasted against its reverse complementary sequence is also shown.

On page 68, please delete the paragraph beginning on line 21 and ending on page 69, line 17, and replace with the following paragraph:

The plasmids of 2715 selected cDNA clones were collected from data set I. The inserts of the cDNAs were amplified by PCR in a 96-well format using primer pairs specific for the vector ends (for inserts in pBluescript SK-: T7, 5′-GTAATACGACTCACTATAGGGC (SEQ ID NO: 55), and 5′ extended M13 reverse, 5′-ACAGGAAACAGCTATGACCATG (SEQ ID NO: 56); for inserts in pZipLox1: M13 forward, 5′-CCCAGTCACGACGTTGTAAAACG (SEQ ID NO: 57) and M13 reverse, 5′-AGCGGATAACAATTTCACACAGG (SEQ ID NO: 58). PCR reactions of 100 μL volume contained 0.4 μM of each primer, 0.2 μM of each desoxynucleotide, 10 mM Tris, 50 mM

KCl, 3.0 mM $MgCl_2$, 3 U *Taq* DNA polymerase (Promega, Madison) and ~10 ng plasmid template. The reactions were run on a Perkin Elmer 9700 Thermoblock using an amplification program of 3 min denaturation at 94 °C, 5 precycles of 30 s at 94 °C, 30 s at 64 °C, 2 min at 72 °C, followed by 30 cycles of 30 s at 94 °C, 30 s at 60 °C, 2 min at 72 °C and terminated by 7 min extension at 72 °C. The PCR products were precipitated by adding 200 µL ethanol (95%) and 10 µL sodium acetate (3M, pH 5.2) and centrifugation at 3200 g and 4 °C for 60 min. After washing with 80% ethanol, the DNA was resuspended in 20 µL 3x SSC. The yield and purity of the PCR products was analyzed by agarose gel electrophoresis. PCR samples showing by agarose gel analysis concentrations less than 0.2 µg/µL and/or double bands were repeated. If possible, alternative clones from the cDNA clone collection were used to repeat the PCR experiments. To reduce the cross-contamination risk in the 96-well format, failed PCRs were not removed from the sample set, and as a result the number of PCR samples for printing increased by approximately 20%.

On page 74, please delete the paragraph beginning on line 19 and ending on line 28, and replace with the following paragraph:

Control vectors contained a GUS expression vector with either a napin or phaseolin promoter. For example, the promoter region of the napin (napA) gene in Brassica napus was amplified by using a forward primer CG aagctt TCTTCATCGGTGATT (SEQ ID NO: 59) and reverse primer GGTCG gaattc GTGTATGTTTT (SEQ ID NO: 60). The PCR product was digested by Hind III and EcoR I, then inserted into SK+ vector and confirmed by sequencing. The napin promoter was cut by Hind III and BamH I and inserted into a GUS expression vector such that GUS is under control of the napin promoter region. In a similar fashion, a GUS expression vector under control of a phaseolin promoter region was constructed; the phaseolin promoter region is described in patent US 5,504,200.

Table 3. Primers for the PCR amplification of 12 promoter regions

name	sequence	position	REs	T(°C)	Length 1	Length2
1R	CACT GGATCC **TTTTTGTTTGTTGTGAGAGATG** (SEQ ID NO: 31)	best+3	Bam	48	23	32
1F	CACT GAATTC **ACAAACATACACTCAAAATC** (SEQ ID NO: 32)	best	Eco	48	21	30
3R	CACT GGATCC **GTTTTGCTATTTGTGTATGTTTTC** (SEQ ID NO: 33)	best+0	Bam	48	24	34
3F	CACT GAATTC **AAGAGTGTAAAACGTAC** (SEQ ID NO: 34)	best	Eco	48	18	27
4R2	CACT GGATC **C TTGTTGTTTTGTTGATGTGTT** (SEQ ID NO: 35)	best+5	Bam	48	22	31
4F2	CACT GAATT **C CATTGTTTACACGTC** (SEQ ID NO: 36)	best	Eco	48	16	25
6R	CACT GGATCC **GGGTGTGTTTTGTTTTGTATAAG** (SEQ ID NO: 37)	best+4	Bam	52	23	33
6F	CACT GAATT **C TAAACGAGTAAAGTTTAGCAC** (SEQ ID NO: 38)	best	Eco	52	22	31
7R	CACT GGATC **C TATGTGTGTATGTTTTGGTTC** (SEQ ID NO: 39)	best+6	Bam	52	22	31

Figure 19a

name	sequence	position	REs	T(°C)	Length 1	Length2
7F	CACT GAATTC **GATCCGAAAAGTAGAGTTTC** (SEQ ID NO: 40)	best	Eco	52	20	30
9R2	CACT GGATC **C TTTTGATTTTTTGGATTAGATTGTGTTTGTGGT** (SEQ ID NO: 41)	nb+0	Bam	52	34	43
9F	CACT GAAT **TC AGAAAGAGAAGTGAGC** (SEQ ID NO: 42)	best	Eco	52	18	26
13R	CACT GGA **TCC GGCGAAGGTTGATATGA** (SEQ ID NO: 43)	best+4	Bam	60	20	27
13F	CACT CAAT **TG ACACGCAACAACCAAAGC** (SEQ ID NO: 44)	best	Mfe	60	20	28
14R	CACT GGATC **C GGAGAAAGAGAAAGAGAT** (SEQ ID NO: 45)	best+8	Bam	52	19	28
14F	CACT GAATT **C ATCTCTGCAAATCAAACC** (SEQ ID NO: 46)	best	Eco	52	19	28
15R	CACT GGATC **C TCGCTCTTAATTTGTTATGC** (SEQ ID NO: 47)	best+5	Bam	52	21	30
15F	CACT CAATT **G TAAGTCGTTCTCTAATCTTC** (SEQ ID NO: 48)	best	Mfe	52	21	30
16R	CACT GGATCC **GCATCAAGGACTATACTTCAC** (SEQ ID NO: 49)	best+0	Bam	56	21	31

Figure 19b

name	sequence	position	REs	T(°C)	Length 1	Length2
16F	CACT GAATTC **GTGAGAAAATTCATGAGCACTC** (SEQ ID NO: 50)	best	Eco	56	22	32
17R	CACT GGATCC **GTTTCCCACTCTCTCC** (SEQ ID NO: 51)	best+0	Bam	56	16	26
17F	CACT GAATT C **AAACGAGGCTCCAAATTC** (SEQ ID NO: 52)	best	Eco	56	19	28
19R	CACT GGATCC **GTTGACTTGAAGACAAGC** (SEQ ID NO: 53)	best+1	Bam	52	18	28
19F	CACT GAATT C **ACCAAGCCTATACAAAC** (SEQ ID NO: 54)	best	Eco	52	18	27

Position: Distance from the best position (for reverse primers, it is ATG)

REs : Restriction enzyme sites included

T(°C): Anealling tempeture

Length 1: Length of the sequences exist in genomic sequences

Length 2: Full length

Figure 19c